SEQUENCE LISTING

<110> Curtis, Rory A.J., Lora, Jose M.

<120> 46798, A HUMAN MATRIX METALLOPROTEINASE
      AND USES THEREFOR

<130> MPI2001-014P1RCP1(M)

<150> 60/262,252

<151> 2001-01-16

<160> 10

<170> FastSEQ for Windows Version 3.0

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<213> Homo sapiens

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ccggctcccg gcgaagggca gcggaggagc ggcccagagc gcgcagctag ggcactggcg 180
aaaccccggg acagtccctc tccgtgcggg ggcggcgcag agcagtccca tccccggggt 240
cccgggcgcg gctgactgcc ggctggttcc ctgcgcgcag tagctccccg agccgggctg 300
caccggaggc ggcgag atg gtc gcg cgc gtc ggc ctc ctg ctg cgc gcc ctg 352
                    Met Val Ala Arg Val Gly Leu Leu Leu Arg Ala Leu
                     1   5   10

cag ctg cta ctg tgg ggc cac ctg gac gcc cag ccc gcg gag cgc gga   400
Gln Leu Leu Leu Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly
         15   20   25

ggc cag gag ctg cgc aag gag gcg gag gca ttc cta gag aag tac gga   448
Gly Gln Glu Leu Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly
     30   35   40

tac ctc aat gaa cag gtc ccc aaa gct ccc acc tcc act cga ttc agc   496
Tyr Leu Asn Glu Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser
 45   50   55   60

gat gcc atc aga gcg ttt cag tgg gtg tcc cag cta cct gtc agc ggc   544
Asp Ala Ile Arg Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly
                 65   70   75

gtg ttg gac cgc gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggg   592
Val Leu Asp Arg Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly
                 80   85   90

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gtt aca gat acc aac agt tat gcg gcc tgg gct gag agg atc agt gac      640
Val Thr Asp Thr Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp
        95                  100                 105

ttg ttt gct aga cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca      688
Leu Phe Ala Arg His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala
        110                 115                 120

aag caa ggg ggc gcc ctg gcg cac gcc ttc ctg ccc cgc cgc ggc gaa      736
Lys Gln Gly Gly Ala Leu Ala His Ala Phe Leu Pro Arg Arg Gly Glu
125                 130                 135                 140

gcg cac ttc gac caa gat gag cgc tgg tcc ctg agc cgc cgc cgc ggg      784
Ala His Phe Asp Gln Asp Glu Arg Trp Ser Leu Ser Arg Arg Arg Gly
                145                 150                 155


cgc aac ctg ttc gtg gtg ctg gcg cac gag atc ggt cac acg ctt ggc      832
Arg Asn Leu Phe Val Val Leu Ala His Glu Ile Gly His Thr Leu Gly
            160                 165                 170

ctc acc cac tcg ccc gcg ccg cgc gcg ctc atg gcg ccc tac tac aag      880
Leu Thr His Ser Pro Ala Pro Arg Ala Leu Met Ala Pro Tyr Tyr Lys
            175                 180                 185

agg ctg ggc cgc gac gcg ctg ctc agc tgg gac gac gtg ctg gcc gtg      928
Arg Leu Gly Arg Asp Ala Leu Leu Ser Trp Asp Asp Val Leu Ala Val
            190                 195                 200

cag agc ctg tat ggg aag ccc cta ggg ggc tca gtg gcc gtc cag ctc      976
Gln Ser Leu Tyr Gly Lys Pro Leu Gly Gly Ser Val Ala Val Gln Leu
205                 210                 215                 220

cca gga aag ctg ttc act gac ttt gag acc tgg gac tcc tac agc ccc      1024
Pro Gly Lys Leu Phe Thr Asp Phe Glu Thr Trp Asp Ser Tyr Ser Pro
                225                 230                 235

caa gga agg cgc cct gaa acg cag ggc cct aaa tac tgc cac tct tcc      1072
Gln Gly Arg Arg Pro Glu Thr Gln Gly Pro Lys Tyr Cys His Ser Ser
            240                 245                 250

ttc gat gcc atc act gta gac agg caa cag caa ctg tac att ttt aaa      1120
Phe Asp Ala Ile Thr Val Asp Arg Gln Gln Gln Leu Tyr Ile Phe Lys
            255                 260                 265

ggg agc cat ttc tgg gag gtg gca gct gat ggc aac gtc tca gag ccc      1168
Gly Ser His Phe Trp Glu Val Ala Ala Asp Gly Asn Val Ser Glu Pro
            270                 275                 280

cgt cca ctg cag gaa aga tgg gtc ggg ctg ccc ccc aac att gag gct      1216
Arg Pro Leu Gln Glu Arg Trp Val Gly Leu Pro Pro Asn Ile Glu Ala
285                 290                 295                 300

gcg gca gtg tca ttg aat gat gga gat ttc tac ttc ttc aaa ggg ggt      1264
Ala Ala Val Ser Leu Asn Asp Gly Asp Phe Tyr Phe Phe Lys Gly Gly
                305                 310                 315
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cga tgc tgg agg ttc cgg ggc ccc aag cca gtg tgg ggt ctc cca cag   1312
Arg Cys Trp Arg Phe Arg Gly Pro Lys Pro Val Trp Gly Leu Pro Gln
        320             325             330

ctg tgc cgg gca ggg ggc ctg ccc cgc cat cct gac gcc gcc ctc ttc   1360
Leu Cys Arg Ala Gly Gly Leu Pro Arg His Pro Asp Ala Ala Leu Phe
        335             340             345

ttc cct cct ctg cgc cgc ctc atc ctc ttc aag ggt gcc cgc tac tac   1408
Phe Pro Pro Leu Arg Arg Leu Ile Leu Phe Lys Gly Ala Arg Tyr Tyr
        350             355             360

gtg ctg gcc cga ggg gga ctg caa gtg gag ccc tac tac ccc cga agt   1456
Val Leu Ala Arg Gly Gly Leu Gln Val Glu Pro Tyr Tyr Pro Arg Ser
365             370             375             380

ctg cag gac tgg gga ggc atc cct gag gag gtc agc ggc gcc ctg ccg   1504
Leu Gln Asp Trp Gly Gly Ile Pro Glu Glu Val Ser Gly Ala Leu Pro
                385             390             395

agg ccc gat ggc tcc atc atc ttc ttc cga gat gac cgc tac tgg cgc   1552
Arg Pro Asp Gly Ser Ile Ile Phe Phe Arg Asp Asp Arg Tyr Trp Arg
                400             405             410

ctc gac cag gcc aaa ctg cag gca acc acc tcg ggc cgc tgg gcc acc   1600
Leu Asp Gln Ala Lys Leu Gln Ala Thr Thr Ser Gly Arg Trp Ala Thr
        415             420             425

gag ctg ccc tgg atg ggc tgc tgg cat gcc aac tcg ggg agc gcc ctg   1648
Glu Leu Pro Trp Met Gly Cys Trp His Ala Asn Ser Gly Ser Ala Leu
        430             435             440

ttc tgaaggcacc tcctcacctc agaaactggt ggtgctctca gggcaaaatc        1701
Phe
445

atgttcccca cccccggggc agaacccctc ttagaagcct ctgagtccct ctgcagaaga 1761
ccgggcagca aagcctccat ctggaagtct gtctgccttt gttccttgaa gaatgcagca 1821
ttgtctttgt ctgtccccac cacatggagg tgggggtggg atcaatctta ggaaaagcaa 1881
aaaagggtcc cagatccctt ggccctttcc tccgaggact tctatcctcc ccaggccttt 1941
gtttcttcgg ctaaaggtac agttcctttc aagaggtaac agcactggga tccaagcagg 2001
gggatgaaaa actcagcaga gaaattcgag accattttgc aagactgtgc ccttctcctc 2061
aggacccct ggctcagttc ttgaaaaacg gtgtcatatt tagtcagagg ccccacccc  2121
aggaagcatg gatggggatg aaggcacagg cgtctccaac ctcagaggcc ctttgtgggg 2181
tcaggacaca gagtgggagg gagactgatg caggcctacc agtccctggc tttttgtctg 2241
gggctggaat aaagaggtgc cttcagctgg tgggccgaga aaaaaaaaa aaaaaaaag  2301
ggcggccgc                                                        2310


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        <213> Homo sapiens

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             20                          25                          30
Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly Tyr Leu Asn Glu
         35                          40                          45
Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg
     50                          55                          60
Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly Val Leu Asp Arg
65                          70                          75                      80
Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly Val Thr Asp Thr
                 85                          90                          95
Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg
             100                         105                         110
His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Lys Gln Gly Gly
         115                         120                         125
Ala Leu Ala His Ala Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp
     130                         135                         140
Gln Asp Glu Arg Trp Ser Leu Ser Arg Arg Arg Gly Arg Asn Leu Phe
145                         150                         155                     160
Val Val Leu Ala His Glu Ile Gly His Thr Leu Gly Leu Thr His Ser
                 165                         170                         175
Pro Ala Pro Arg Ala Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg
             180                         185                         190
Asp Ala Leu Leu Ser Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr
         195                         200                         205
Gly Lys Pro Leu Gly Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu
     210                         215                         220
Phe Thr Asp Phe Glu Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg
225                         230                         235                     240
Pro Glu Thr Gln Gly Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile
                 245                         250                         255
Thr Val Asp Arg Gln Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe
             260                         265                         270
Trp Glu Val Ala Ala Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln
         275                         280                         285
Glu Arg Trp Val Gly Leu Pro Pro Asn Ile Glu Ala Ala Ala Val Ser
     290                         295                         300
Leu Asn Asp Gly Asp Phe Tyr Phe Phe Lys Gly Gly Arg Cys Trp Arg
305                         310                         315                     320
Phe Arg Gly Pro Lys Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala
                 325                         330                         335
Gly Gly Leu Pro Arg His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu
             340                         345                         350
Arg Arg Leu Ile Leu Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg
         355                         360                         365
Gly Gly Leu Gln Val Glu Pro Tyr Tyr Pro Arg Ser Leu Gln Asp Trp
     370                         375                         380
Gly Gly Ile Pro Glu Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly
385                         390                         395                     400
Ser Ile Ile Phe Phe Arg Asp Asp Arg Tyr Trp Arg Leu Asp Gln Ala
                 405                         410                         415
Lys Leu Gln Ala Thr Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp
             420                         425                         430
Met Gly Cys Trp His Ala Asn Ser Gly Ser Ala Leu Phe
         435                         440                         445

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<211> 1335
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1335)

<400> 3

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tgg ggc cac ctg gac gcc cag ccc gcg gag cgc gga ggc cag gag ctg
                20                  25                  30
Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly Gly Gln Glu Leu

cgc aag gag gcg gag gca ttc cta gag aag tac gga tac ctc aat gaa
            35                  40                  45
Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly Tyr Leu Asn Glu

cag gtc ccc aaa gct ccc acc tcc act cga ttc agc gat gcc atc aga
        50                  55                  60
Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg

gcg ttt cag tgg gtg tcc cag cta cct gtc agc ggc gtg ttg gac cgc
65                  70                  75                  80
Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly Val Leu Asp Arg

gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggg gtt aca gat acc
                85                  90                  95
Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly Val Thr Asp Thr

aac agt tat gcg gcc tgg gct gag agg atc agt gac ttg ttt gct aga
                100                 105                 110
Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg

cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca aag caa ggg ggc
            115                 120                 125
His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Lys Gln Gly Gly

gcc ctg gcg cac gcc ttc ctg ccc cgc cgc ggc gaa gcg cac ttc gac
    130                 135                 140
Ala Leu Ala His Ala Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp

caa gat gag cgc tgg tcc ctg agc cgc cgc cgc ggg cgc aac ctg ttc
145                 150                 155                 160
Gln Asp Glu Arg Trp Ser Leu Ser Arg Arg Arg Gly Arg Asn Leu Phe

gtg gtg ctg gcg cac gag atc ggt cac acg ctt ggc ctc acc cac tcg
                165                 170                 175
Val Val Leu Ala His Glu Ile Gly His Thr Leu Gly Leu Thr His Ser


ccc gcg ccg cgc gcg ctc atg gcg ccc tac tac aag agg ctg ggc cgc
                180                 185                 190
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Pro Ala Pro Arg Ala Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg

gac gcg ctg ctc agc tgg gac gac gtg ctg gcc gtg cag agc ctg tat
        195                 200                 205
Asp Ala Leu Leu Ser Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr

ggg aag ccc cta ggg ggc tca gtg gcc gtc cag ctc cca gga aag ctg
        210                 215                 220
Gly Lys Pro Leu Gly Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu

ttc act gac ttt gag acc tgg gac tcc tac agc ccc caa gga agg cgc
 225                 230                 235                 240
Phe Thr Asp Phe Glu Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg

cct gaa acg cag ggc cct aaa tac tgc cac tct tcc ttc gat gcc atc
                245                 250                 255
Pro Glu Thr Gln Gly Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile

act gta gac agg caa cag caa ctg tac att ttt aaa ggg agc cat ttc
            260                 265                 270
Thr Val Asp Arg Gln Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe

tgg gag gtg gca gct gat ggc aac gtc tca gag ccc cgt cca ctg cag
            275                 280                 285
Trp Glu Val Ala Ala Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln

gaa aga tgg gtc ggg ctg ccc ccc aac att gag gct gcg gca gtg tca
    290                 295                 300
Glu Arg Trp Val Gly Leu Pro Pro Asn Ile Glu Ala Ala Ala Val Ser

ttg aat gat gga gat ttc tac ttc ttc aaa ggg ggt cga tgc tgg agg
 305                 310                 315                 320
Leu Asn Asp Gly Asp Phe Tyr Phe Phe Lys Gly Gly Arg Cys Trp Arg

ttc cgg ggc ccc aag cca gtg tgg ggt ctc cca cag ctg tgc cgg gca
            325                 330                 335
Phe Arg Gly Pro Lys Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala

ggg ggc ctg ccc cgc cat cct gac gcc gcc ctc ttc ttc cct cct ctg
            340                 345                 350
Gly Gly Leu Pro Arg His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu

cgc cgc ctc atc ctc ttc aag ggt gcc cgc tac tac gtg ctg gcc cga
            355                 360                 365
Arg Arg Leu Ile Leu Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg

ggg gga ctg caa gtg gag ccc tac tac ccc cga agt ctg cag gac tgg
        370                 375                 380
Gly Gly Leu Gln Val Glu Pro Tyr Tyr Pro Arg Ser Leu Gln Asp Trp

gga ggc atc cct gag gag gtc agc ggc gcc ctg ccg agg ccc gat ggc
 385                 390                 395                 400
Gly Gly Ile Pro Glu Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly

tcc atc atc ttc ttc cga gat gac cgc tac tgg cgc ctc gac cag gcc
                405                 410                 415
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Ser Ile Ile Phe Phe Arg Asp Asp Arg Tyr Trp Arg Leu Asp Gln Ala

aaa ctg cag gca acc acc tcg ggc cgc tgg gcc acc gag ctg ccc tgg
            420   425   430
Lys Leu Gln Ala Thr Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp

atg ggc tgc tgg cat gcc aac tcg ggg agc gcc ctg ttc
            435   440   445
Met Gly Cys Trp His Ala Asn Ser Gly Ser Ala Leu Phe

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Thr Arg Lys Lys Ala Ser Asn Ser Leu Val Glu Lys Leu Lys Glu Met
            20   25   30
Gln Lys Phe Phe Gly Leu Pro Val Thr Gly Lys Leu Asp Ser Asn Thr
        35   40   45
Leu Glu Val Met Lys Lys Pro Arg Cys Gly Val Pro Asp Val Gly Glu
    50   55   60
Phe Arg Thr Phe Pro Gly Ser Pro Lys Trp Ser Lys Asn Asn Leu Leu
65   70   75   80
Thr Tyr Arg Ile Val Asn Tyr Thr Pro Asp Leu Pro Arg Glu Asp Val
            85   90   95
Asp Asp Ala Ile Arg Arg Ala Phe Gln Val Trp Ser Asp Val Thr Pro
            100   105   110
Leu Thr Phe Thr Arg Val Ser Asp Gly Glu Ala Asp Ile Met Ile Ser
        115   120   125
Phe Ala Arg Gly Glu His Gly Asp Phe Tyr Pro Phe Asp Gly Lys Gly
    130   135   140
Gly Leu Leu Ala His Ala Phe Ala Pro Gly Pro Gly Ile Gly Ile Gly
145   150   155   160
Asp Ala His Phe Asp Asp Asp Glu Thr Trp Thr
            165   170

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        <211> 50
        <212> PRT
        <213> Homo sapiens

        <400> 5
Ile Asp Ala Ala Phe Glu Asp Arg Asp Arg Gly Lys Thr Tyr Phe Phe
1   5   10   15
Lys Gly Asp Lys Tyr Trp Arg Phe Asp Pro Glu Thr Arg Gln Arg Val
            20   25   30
Asp Pro Gly Tyr Pro Lys Leu Ile Ser Asp Leu Trp Pro Asp Gly Leu
        35   40   45
Pro Cys
    50

        <210> 6
        <211> 471

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<212> PRT
<213> Homo sapiens

<400> 6

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Cys Arg Ala Leu Pro Leu Pro Ser Gly Gly Asp Glu Asp Asp Leu Ser
            20                  25                  30
Glu Glu Asp Leu Gln Phe Ala Glu Arg Tyr Leu Arg Ser Tyr Tyr His
        35                  40                  45
Pro Thr Asn Leu Ala Gly Ile Leu Lys Glu Asn Ala Ala Ser Ser Met
    50                  55                  60
Thr Glu Arg Leu Arg Glu Met Gln Ser Phe Phe Gly Leu Glu Val Thr
65                  70                  75                  80
Gly Lys Leu Asp Asp Asn Thr Leu Asp Val Met Lys Lys Pro Arg Cys
                85                  90                  95
Gly Val Pro Asp Val Gly Glu Tyr Asn Val Phe Pro Arg Thr Leu Lys
            100                 105                 110
Trp Ser Lys Met Asn Leu Thr Tyr Arg Ile Val Asn Tyr Thr Pro Asp
        115                 120                 125
Met Thr His Ser Glu Val Glu Lys Ala Phe Lys Lys Ala Phe Lys Val
    130                 135                 140
Trp Ser Asp Val Thr Pro Leu Asn Phe Thr Arg Leu His Asp Gly Ile
145                 150                 155                 160
Ala Asp Ile Met Ile Ser Phe Gly Ile Lys Glu His Gly Asp Phe Tyr
                165                 170                 175
Pro Phe Asp Gly Pro Ser Gly Leu Leu Ala His Ala Phe Pro Pro Gly
            180                 185                 190
Pro Asn Tyr Gly Gly Asp Ala His Phe Asp Asp Asp Glu Thr Trp Thr
            195                 200                 205
Ser Ser Ser Lys Gly Tyr Asn Leu Phe Leu Val Ala Ala His Glu Phe
    210                 215                 220
Gly His Ser Leu Gly Leu Asp His Ser Lys Asp Pro Gly Ala Leu Met
225                 230                 235                 240
Phe Pro Ile Tyr Thr Tyr Thr Gly Lys Ser His Phe Met Leu Pro Asp
                245                 250                 255
Asp Asp Val Gln Gly Ile Gln Ser Leu Tyr Gly Pro Gly Asp Glu Asp
            260                 265                 270
Pro Asn Pro Lys His Pro Lys Thr Pro Asp Lys Cys Asp Pro Ser Leu
    275                 280                 285
Ser Leu Asp Ala Ile Thr Ser Leu Arg Gly Glu Thr Met Ile Phe Lys
    290                 295                 300
Asp Arg Phe Phe Trp Arg Leu His Pro Gln Gln Val Asp Ala Glu Leu
305                 310                 315                 320
Phe Leu Thr Lys Ser Phe Trp Pro Glu Leu Pro Asn Arg Ile Asp Ala
            325                 330                 335
Ala Tyr Glu His Pro Ser His Asp Leu Ile Phe Ile Phe Arg Gly Arg
            340                 345                 350
Lys Phe Trp Ala Leu Asn Gly Tyr Asp Ile Leu Glu Gly Tyr Pro Lys
        355                 360                 365
Lys Ile Ser Glu Leu Gly Leu Pro Lys Glu Val Lys Lys Ile Ser Ala
    370                 375                 380
Ala Val His Phe Glu Asp Thr Gly Lys Thr Leu Leu Phe Ser Gly Asn
385                 390                 395                 400
Gln Val Trp Arg Tyr Asp Asp Thr Asn His Ile Met Asp Lys Asp Tyr
            405                 410                 415
Pro Arg Leu Ile Glu Glu Asp Phe Pro Gly Ile Gly Asp Lys Val Asp
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                    420                  425                  430
    Ala Val Tyr Glu Lys Asn Gly Tyr Ile Tyr Phe Phe Asn Gly Pro Ile
            435                  440                  445
    Gln Phe Glu Tyr Ser Ile Trp Ser Asn Arg Ile Val Arg Val Met Pro
        450              455                  460
    Ala Asn Ser Ile Leu Trp Cys
    465              470
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            <211> <210> 7
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (1)...(1)
<223> The amino acid at position 1 can be G, S, T, A, L,
      I, V, N.

<223> Xaa at position 2 and 3 = any amino acid

<221> VARIANT
<222> (6)...(6)
<223> The amino acid at position 6 can be L, I, V, M, F,
      Y, W.

<221> VARIANT
<222> (7)...(7)
<223> The  amino acid at position 7 can not be D, E, H,
      R, K, P.

<223> Xaa at position 9= any amino acid

<221> VARIANT
<222> (10)...(10)
<223> The amino acid at position 10 can be L, I, V, M,
      F, Y, W, G, S, P, Q.

<400> 4
Xaa Xaa Xaa His Glu Xaa Xaa His Xaa Xaa
 1               5                   10




<210> 8
<211> 2527
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (300)...(1862)

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gcggacccgc gggcaggcac tgcccgggct ggacgacgtc tggccggctc ccggcgaagg 120
gcagcggagg agcggcccag agcgcgcagc tagggcactg cgaaacccc gggacagtcc 180
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ctctccgtgc gggggcggcg cagagcagtc ccatccccgg ggtcccgggc.gcggctgact 240
gccggctggt tccctgcgcg cagtagctcc ccgagccggg ctgcaccgga ggcggcgag 299
atg gtc gcg cgc gtc ggc ctc ctg ctg cgc gcc ctg cag ctg cta ctg 347
Met Val Ala Arg Val Gly Leu Leu Leu Arg Ala Leu Gln Leu Leu Leu
1               5                   10                  15

tgg ggc cac ctg gac gcc cag ccc gcg gag cgc gga ggc cag gag ctg 395
Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly Gly Gln Glu Leu
            20                  25                  30

cgc aag gag gcg gag gca ttc cta gag aag tac gga tac ctc aat gaa 443
Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly Tyr Leu Asn Glu
        35                  40                  45

cag gtc ccc aaa gct ccc acc tcc act cga ttc agc gat gcc atc aga 491
Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg
        50                  55                  60

gcg ttt cag tgg gtg tcc cag cta cct gtc agc ggc gtg ttg gac cgc 539
Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly Val Leu Asp Arg
65                  70                  75                  80

gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggg gtt aca gat acc 587
Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly Val Thr Asp Thr
                85                  90                  95

aac agt tat gcg gcc tgg gct gag agg atc agt gac ttg ttt gct aga 635
Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg
            100                 105                 110

cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca aag caa ggt aac 683
His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Lys Gln Gly Asn
        115                 120                 125

aaa tgg tac aag cag cac ctc tcc tac cgc ctg gtg aac tgg cct gag 731
Lys Trp Tyr Lys Gln His Leu Ser Tyr Arg Leu Val Asn Trp Pro Glu
        130                 135                 140

cat ctg ccg gag ccg gca gtt cgg ggc gcc gtg cgc gcc gcc ttc cag 779
His Leu Pro Glu Pro Ala Val Arg Gly Ala Val Arg Ala Ala Phe Gln
145                 150                 155                 160

ttg tgg agc aac gtc tca gcg ctg gag ttc tgg gag gcc cca gcc aca 827
Leu Trp Ser Asn Val Ser Ala Leu Glu Phe Trp Glu Ala Pro Ala Thr
            165                 170                 175

ggc ccc gct gac atc cgg ctc acc ttc ttc caa ggg gac cac aac gat 875
Gly Pro Ala Asp Ile Arg Leu Thr Phe Phe Gln Gly Asp His Asn Asp
            180                 185                 190

ggg ctg ggc aat gcc ttt gat ggc cca ggg ggc gcc ctg gcg cac gcc 923
Gly Leu Gly Asn Ala Phe Asp Gly Pro Gly Gly Ala Leu Ala His Ala
            195                 200                 205

ttc ctg ccc cgc cgc ggc gaa gcg cac ttc gac caa gat gag cgc tgg 971
Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp Gln Asp Glu Arg Trp
        210                 215                 220
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            145                      150                      155                         160
Leu Trp Ser Asn Val Ser Ala Leu Glu Phe Trp Glu Ala Pro Ala Thr
                    165                      170                      175
Gly Pro Ala Asp Ile Arg Leu Thr Phe Phe Gln Gly Asp His Asn Asp
                    180                      185                      190
Gly Leu Gly Asn Ala Phe Asp Gly Pro Gly Gly Ala Leu Ala His Ala
                    195                      200                      205
Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp Gln Asp Glu Arg Trp
        210                      215                      220
Ser Leu Ser Arg Arg Arg Gly Arg Asn Leu Phe Val Val Leu Ala His
225                      230                      235                         240
Glu Ile Gly His Thr Leu Gly Leu Thr His Ser Pro Ala Pro Arg Ala
                    245                      250                      255
Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg Asp Ala Leu Leu Ser
                    260                      265                      270
Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr Gly Lys Pro Leu Gly
                    275                      280                      285
Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu Phe Thr Asp Phe Glu
                    290                      295                      300
Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg Pro Glu Thr Gln Gly
305                      310                      315                         320
Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile Thr Val Asp Arg Gln
                    325                      330                      335
Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe Trp Glu Val Ala Ala
                    340                      345                      350
Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln Glu Arg Trp Val Gly
                    355                      360                      365
Leu Pro Pro Asn Ile Glu Ala Ala Ala Val Ser Leu Asn Asp Gly Asp
        370                      375                      380
Phe Tyr Phe Phe Lys Gly Gly Arg Cys Trp Arg Phe Arg Gly Pro Lys
385                      390                      395                         400
Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala Gly Gly Leu Pro Arg
                    405                      410                      415
His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu Arg Arg Leu Ile Leu
                    420                      425                      430
Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg Gly Gly Leu Gln Val
                    435                      440                      445
Glu Pro Tyr Tyr Pro Arg Ser Leu Gln Asp Trp Gly Gly Ile Pro Glu
        450                      455                      460
Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly Ser Ile Ile Phe Phe
465                      470                      475                         480
Arg Asp Asp Arg Tyr Trp Arg Leu Asp Gln Ala Lys Leu Gln Ala Thr
                    485                      490                      495
Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp Met Gly Cys Trp His
                    500                      505                      510
Ala Asn Ser Gly Ser Ala Leu Phe
        515                      520
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Met Val Ala Arg Val Gly Leu Leu Leu Arg Ala Leu Gln Leu Leu Leu
 1               5                  10                  15

tgg ggc cac ctg gac gcc cag ccc gcg gag cgc gga ggc cag gag ctg     96
Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly Gly Gln Glu Leu
                20                  25                  30

cgc aag gag gcg gag gca ttc cta gag aag tac gga tac ctc aat gaa    144
Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly Tyr Leu Asn Glu
            35                  40                  45

cag gtc ccc aaa gct ccc acc tcc act cga ttc agc gat gcc atc aga    192
Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg
        50                  55                  60

gcg ttt cag tgg gtg tcc cag cta cct gtc agc ggc gtg ttg gac cgc    240
Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly Val Leu Asp Arg
 65                  70                  75                  80

gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggg gtt aca gat acc    288
Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly Val Thr Asp Thr
                85                  90                  95

aac agt tat gcg gcc tgg gct gag agg atc agt gac ttg ttt gct aga    336
Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg
            100                 105                 110

cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca aag caa ggt aac    384
His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Lys Gln Gly Asn
            115                 120                 125

aaa tgg tac aag cag cac ctc tcc tac cgc ctg gtg aac tgg cct gag    432
Lys Trp Tyr Lys Gln His Leu Ser Tyr Arg Leu Val Asn Trp Pro Glu
        130                 135                 140

cat ctg ccg gag ccg gca gtt cgg ggc gcc gtg cgc gcc gcc ttc cag    480
His Leu Pro Glu Pro Ala Val Arg Gly Ala Val Arg Ala Ala Phe Gln
145                 150                 155                 160

ttg tgg agc aac gtc tca gcg ctg gag ttc tgg gag gcc cca gcc aca    528
Leu Trp Ser Asn Val Ser Ala Leu Glu Phe Trp Glu Ala Pro Ala Thr
                165                 170                 175

ggc ccc gct gac atc cgg ctc acc ttc ttc caa ggg gac cac aac gat    576
Gly Pro Ala Asp Ile Arg Leu Thr Phe Phe Gln Gly Asp His Asn Asp
                180                 185                 190

ggg ctg ggc aat gcc ttt gat ggc cca ggg ggc gcc ctg gcg cac gcc    624
Gly Leu Gly Asn Ala Phe Asp Gly Pro Gly Gly Ala Leu Ala His Ala
            195                 200                 205

ttc ctg ccc cgc cgc ggc gaa gcg cac ttc gac caa gat gag cgc tgg    672
Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp Gln Asp Glu Arg Trp
        210                 215                 220
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tcc ctg agc cgc cgc cgc ggg cgc aac ctg ttc gtg gtg ctg gcg cac      1019
Ser Leu Ser Arg Arg Arg Gly Arg Asn Leu Phe Val Val Leu Ala His
225                 230                 235                 240

gag atc ggt cac acg ctt ggc ctc acc cac tcg ccc gcg ccg cgc gcg      1067
Glu Ile Gly His Thr Leu Gly Leu Thr His Ser Pro Ala Pro Arg Ala
                245                 250                 255

ctc atg gcg ccc tac tac aag agg ctg ggc cgc gac gcg ctg ctc agc      1115
Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg Asp Ala Leu Leu Ser
                260                 265                 270

tgg gac gac gtg ctg gcc gtg cag agc ctg tat ggg aag ccc cta ggg      1163
Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr Gly Lys Pro Leu Gly
                275                 280                 285

ggc tca gtg gcc gtc cag ctc cca gga aag ctg ttc act gac ttt gag      1211
Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu Phe Thr Asp Phe Glu
                290                 295                 300

acc tgg gac tcc tac agc ccc caa gga agg cgc cct gaa acg cag ggc      1259
Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg Pro Glu Thr Gln Gly
305                 310                 315                 320

cct aaa tac tgc cac tct tcc ttc gat gcc atc act gta gac agg caa      1307
Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile Thr Val Asp Arg Gln
                325                 330                 335

cag caa ctg tac att ttt aaa ggg agc cat ttc tgg gag gtg gca gct      1355
Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe Trp Glu Val Ala Ala
                340                 345                 350

gat ggc aac gtc tca gag ccc cgt cca ctg cag gaa aga tgg gtc ggg      1403
Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln Glu Arg Trp Val Gly
                355                 360                 365

ctg ccc ccc aac att gag gct gcg gca gtg tca ttg aat gat gga gat      1451
Leu Pro Pro Asn Ile Glu Ala Ala Ala Val Ser Leu Asn Asp Gly Asp
                370                 375                 380

ttc tac ttc ttc aaa ggg ggt cga tgc tgg agg ttc cgg ggc ccc aag      1499
Phe Tyr Phe Phe Lys Gly Gly Arg Cys Trp Arg Phe Arg Gly Pro Lys
385                 390                 395                 400

cca gtg tgg ggt ctc cca cag ctg tgc cgg gca ggg ggc ctg ccc cgc      1547
Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala Gly Gly Leu Pro Arg
                405                 410                 415

cat cct gac gcc gcc ctc ttc ttc cct cct ctg cgc cgc ctc atc ctc      1595
His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu Arg Arg Leu Ile Leu
                420                 425                 430

ttc aag ggt gcc cgc tac tac gtg ctg gcc cga ggg gga ctg caa gtg      1643
Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg Gly Gly Leu Gln Val
                435                 440                 445
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tcc ctg agc cgc cgc cgc ggg cgc aac ctg ttc gtg gtg ctg gcg cac    720
Ser Leu Ser Arg Arg Arg Gly Arg Asn Leu Phe Val Val Leu Ala His
225                 230                 235                 240

gag atc ggt cac acg ctt ggc ctc acc cac tcg ccc gcg ccg cgc gcg    768
Glu Ile Gly His Thr Leu Gly Leu Thr His Ser Pro Ala Pro Arg Ala
                245                 250                 255

ctc atg gcg ccc tac tac aag agg ctg ggc cgc gac gcg ctg ctc agc    816
Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg Asp Ala Leu Leu Ser
                260                 265                 270

tgg gac gac gtg ctg gcc gtg cag agc ctg tat ggg aag ccc cta ggg    864
Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr Gly Lys Pro Leu Gly
                275                 280                 285

ggc tca gtg gcc gtc cag ctc cca gga aag ctg ttc act gac ttt gag    912
Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu Phe Thr Asp Phe Glu
                290                 295                 300

acc tgg gac tcc tac agc ccc caa gga agg cgc cct gaa acg cag ggc    960
Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg Pro Glu Thr Gln Gly
305                 310                 315                 320

cct aaa tac tgc cac tct tcc ttc gat gcc atc act gta gac agg caa   1008
Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile Thr Val Asp Arg Gln
                325                 330                 335

cag caa ctg tac att ttt aaa ggg agc cat ttc tgg gag gtg gca gct   1056
Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe Trp Glu Val Ala Ala
                340                 345                 350

gat ggc aac gtc tca gag ccc cgt cca ctg cag gaa aga tgg gtc ggg   1104
Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln Glu Arg Trp Val Gly
                355                 360                 365

ctg ccc ccc aac att gag gct gcg gca gtg tca ttg aat gat gga gat   1152
Leu Pro Pro Asn Ile Glu Ala Ala Ala Val Ser Leu Asn Asp Gly Asp
                370                 375                 380

ttc tac ttc ttc aaa ggg ggt cga tgc tgg agg ttc cgg ggc ccc aag   1200
Phe Tyr Phe Phe Lys Gly Gly Arg Cys Trp Arg Phe Arg Gly Pro Lys
385                 390                 395                 400

cca gtg tgg ggt ctc cca cag ctg tgc cgg gca ggg ggc ctg ccc cgc   1248
Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala Gly Gly Leu Pro Arg
                405                 410                 415

cat cct gac gcc gcc ctc ttc ttc cct cct ctg cgc cgc ctc atc ctc   1296
His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu Arg Arg Leu Ile Leu
                420                 425                 430

ttc aag ggt gcc cgc tac tac gtg ctg gcc cga ggg gga ctg caa gtg   1344
Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg Gly Gly Leu Gln Val
                435                 440                 445
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gag ccc tac tac ccc cga agt ctg cag gac tgg gga ggc atc cct gag    1392
Glu Pro Tyr Tyr Pro Arg Ser Leu Gln Asp Trp Gly Gly Ile Pro Glu
    450             455             460

gag gtc agc ggc gcc ctg ccg agg ccc gat ggc tcc atc atc ttc ttc    1440
Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly Ser Ile Ile Phe Phe
465             470             475             480

cga gat gac cgc tac tgg cgc ctc gac cag gcc aaa ctg cag gca acc    1488
Arg Asp Asp Arg Tyr Trp Arg Leu Asp Gln Ala Lys Leu Gln Ala Thr
            485             490             495

acc tcg ggc cgc tgg gcc acc gag ctg ccc tgg atg ggc tgc tgg cat    1536
Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp Met Gly Cys Trp His
            500             505             510

gcc aac tcg ggg agc gcc ctg ttc tga                                1563
Ala Asn Ser Gly Ser Ala Leu Phe  *
            515             520
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